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(71) Applicant *(for all designated States except US)*: **ISTITUTO ONCOLOGICO ROMAGNOLO COOPERATIVA SOCIALE A R.L.** [IT/IT]; Corso Mazzini, 65, I-47100 Forli (IT).

(72) Inventors; and

(75) Inventors/Applicants *(for US only)*: **CALISTRI, Daniele** [IT/IT]; Istituto Oncologico Romagnolo Cooperativa Sociale A R.L., Corso Mazzini, 65, I-47100 Forli (IT). **RENGUCCI, Claudia** [IT/IT]; Instituto Oncologico Romagnolo Cooperativa SocialeA R.L., Corso Mazzini, 65, I-47100 Forli (IT).

(74) Agents: **BANFI, Paolo** et al.; Bianchetti Bracco Minoja S.r.l., Via Rossini, 8, I-20122 Milano (IT).

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(54) Title: METHOD FOR THE IDENTIFICATION OF COLORECTAL TUMORS

(57) Abstract: Disclosed is a method for the early diagnosis of colorectal carcinoma and determination of pre-cancerous lesions of the colon and rectum based on quantitation of DNA extracted from stool and amplified by PCR techniques.

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METHOD FOR THE IDENTIFICATION OF COLORECTAL TUMORS

This invention relates in general to the diagnosis of tumours in human patients and animals. Specifically, it provides a method and kit for the early diagnosis of colorectal carcinoma and determination of pre-cancerous lesions of the colon and rectum. The method of the invention is based on quantitation of DNA extracted from stool and amplified with PCR techniques.

BACKGROUND OF THE INVENTION

In recent years, a great deal of information has been accumulated on the molecular alterations that take place during the development of tumors, such as gene mutations or genomic rearrangements, highlighting the possibility of detecting tumor alterations in biological fluids and consequently indicating the use of these markers as a valid non invasive diagnostic approach.

A tumor that has been widely investigated with this approach is colorectal cancer, which is one of the most common forms of cancer worldwide, with a clinical outcome varying considerably according to the type of lesion and stage of disease at diagnosis (1-3). An early diagnosis is fundamental to reduce morbidity and mortality as a high percentage of patients diagnosed in the early stages of disease are long-term survivors (4). Moreover, the possibility of detecting pre-malignant lesions makes this tumor an ideal target for screening programs. However, although several screening methods are available, a high percentage of individuals do not participate in colorectal cancer screening programs. There are many reasons for this low compliance, such as a lack of knowledge of the benefits of the available screening methods, especially colonoscopy, as well as the unpleasant and troublesome procedures (5).

Gene mutations in stool, especially K-ras (6-12) and to a lesser extent p53 (13), APC gene (14,15) and microsatellite instability (16), have been

repeatedly investigated. Results have shown the presence of these molecular alterations in stool in only a fraction of patients, due to the relatively low frequency of single marker alterations in colorectal cancer. Multiple mutations have been analyzed in parallel on the same stool sample and this approach has led to improved test sensitivity, but is expensive, time-consuming and cannot easily be applied to screening programs (17-21).

The diagnostic potential of DNA amplification of exfoliated cells in stool has recently been considered. Preliminary evidence (19-21) has shown that the semi-quantitative evaluation of DNA amplification (L-DNA) of some DNA fragments longer than 200 bp detects more than 50% of colorectal cancers, with a very high specificity.

US application No. 20020004206 discloses a genetic assay for identifying a tumor disease from samples containing exfoliated epithelial cells. The patent application describes an assay comprising a step of PCR amplification of Kras, APC and p53 fragments, followed by semi-quantitative determination of the amplified DNA based on gel-staining.

DESCRIPTION OF THE INVENTION

The present invention is based on a novel, accurate and rapid approach to cancer detection, that allows a better discrimination between affected and non-affected individuals.

Specifically, object of the invention is a method for the quantitation of DNA from stool samples, useful for the early diagnosis of tumours and pre-cancerous lesions of the colon and rectum, which comprises the following steps:

1) DNA extraction from stool samples;
2) PCR amplification of at least three, preferably at least eight different DNA fragments with a length exceeding 100 base pairs, using deoxynucleotide triphosphates or primers labelled with

detectable molecules;

3) quantitation of the amplified fragments (amplicons);

4) calculation of the total quantity of different amplicons;

5) comparison of the values obtained in (4) with a reference value.

The DNA extraction can be conducted by conventional techniques using commercially available kits. The DNA fragments amplified in step (2) can span one or more non-overlapping genome regions, including genes and non-coding sequences, provided that the fragment length exceeds 100 bp (base pairs), preferably between 100 and 1000 bp, and more preferably between 100 and 500 bp. The fragments can be amplified separately or simultaneously; in the latter case, the amplification products should be distinguished one another by means of appropriate labelling. For example, the primer oligonucleotides or deoxynucleotide triphosphates used in the amplification reaction may carry detectable markers, such as fluorescent molecules (fluorochromes), preferably HEX (Applied Biosystems), 6-FAM (Applied Biosystems) and TAMRA (Applied Biosystems), or other molecules such as biotin, digoxigenin, fluorescein, rhodamine, Cy3, Cy5, 5-FAM Ned, Vic and Pet. The markers are chemically linked to one or more nucleotides within or at the ends of the primer sequences, preferably on the first nucleotide residue, or to the deoxynucleotide triphosphates present in the PCR reaction mixture.

In a preferred embodiment, the following genome fragments are amplified: exons 5 to 8 of p53 (Gene Bank no. X54156, nt. 13042-13253, 13308-13489, 13986-14124, 14404-14603); genomic regions coding for aminoacids 862-954, 1035-1130, 1288-1402 and 1421-1515 of APC (exon 15 - Gene Bank AF127506, M74088).

In a further preferred embodiment, the amplification products are quantified by automatic DNA sequencers/analysers, preferably using the 3100 Avant Genetic Analyzer® (Applied Biosystems). Other techniques suitable for

fragment amplification according to the invention include immunoenzymatic techniques, real time PCR and chemiluminescence techniques.

The PCR amplification is preferably conducted in the presence of an internal control for the detection of Taq inhibitors. For example, a plasmid containing a sequence, also not human-related, amplifiable with the set of primers used in the amplification of the target DNA, may be added to the PCR reaction mixture. This internal control allows to prevent false negative results due to the presence of Taq inhibitors.

In order to determine the quantity of each amplicon it is necessary to prepare a calibration curve by amplifying known dilutions of genomic DNA or plasmids containing the nucleotide sequences of the target DNA fragments, using the same primers and the same conditions of the test samples. For example, when an automatic fragment sequencer/analyser is used, the AUC (Area Under the Curve) values obtained from the amplification of known quantities of DNA are plotted in a calibration curve; the amounts of DNA in the test samples are then interpolated on the same curve.

The total quantity of the amplification products corresponding to different fragments (i.e. the sum of single amplicon amounts), expressed in weight units, is then compared with a reference or "cut-off" value previously determined on the basis of case series comprising healthy subjects and patients in whom the presence of colorectal tumours or lesions has been established. These cases must include a sufficient number of patients and controls to provide a good confidence interval (CI 95%), preferably at least 50 patients and 50 healthy volunteers.

The accuracy, sensitivity and specificity of the method make it particularly useful in the early diagnosis of colorectal tumours, and in the evaluation of the risk or probability of developing such tumours in persons with pre-cancerous colorectal lesions. Further advantages of the method are its

simplicity, speed and low cost.

Another aspect of the invention relates to a kit suitable for carrying out the method described above. The kit may contain labelled oligonucleotides, thermostable DNA polymerase, solutions and reagents for the performance of a PCR reaction and for a quantitation assay (e.g. the immunoenzyme or fluorimetric method). The kit can also contain instructions on the correct operating method.

Figures 1-3: Examples of FL-DNA analysis

Figures 1a and 1b: DNA extracted from stool samples. The levels of amplification of each sample - expressed in weight units (nanograms) - are determined from the corresponding calibration curves (Fig. 2c). The FL-DNA (Fluorescence long DNA) for each sample is given by the sum of the amounts (ng) of three groups of amplicons: p53 – exons 5-8, APC fragments 1-2 and 3-4.

Figures 2a and 2b: electropherograms obtained by amplification of known DNA amounts. The AUC values are normalized (area/100*ng) and plotted against the DNA amount (1, 2, 5, 10 and 20 ng).

Figure 3: ROC curve of FL-DNA analysis of stool samples from patients and healthy donors.

Material and Methods

DNA Purification

Approximately 4 g of stool were thawed at room temperature. DNA was extracted after a 15-min homogenization with 16 ml of TE-9 buffer pH 9 (0.5 M Tris-HCl, 20 mM EDTA and 10 mM NaCl) by ULTRA-Turrax T25 (Janke & Kunkel GmbH & Co. KG IKA-Labortechnik, Staufen, Germany). After centrifugation at 5,000 g for 15 min, the supernatant was transferred to a tube containing 5 ml of 7.5 M ammonium acetate (M-Medical, Florence, Italy) and 30 ml of 100% ethanol (Carlo Erba, Milan, Italy). DNA was recovered by

centrifugation at 5,000 g for 15 min at room temperature. Stool samples were suspended in 1.6 ml of ASL buffer and DNA was extracted using the QIAamp DNA Stool Kit (QIAGEN, Hilden, Germany).

FL-DNA Analysis

Amplifications of exons 5-8 of p53 and fragments 1-4 of APC exon 15 were carried out on 2 µl of DNA from stool in a total volume of 25 µl containing 0.4 µM of each primer, 200 µM of deoxynucleotide triphosphates, 1× reaction buffer with 3.5 mM MgCl2 and 1 unit of Taq polymerase (QIAGEN). The reaction mixture was subjected to 32 cycles: 60s at 94°C and then 60s at 60 °C for p53 exons, and 58°C for APC fragments, followed by incubation at 72°C for 60s.

The p53 exons were amplified simultaneously in a single reaction mixture and the 4 APC fragments were amplified in two different mixes (mix 1 - fragments 1 and 2; mix 2 - fragments 3 and 4). For this purpose, primers used for L-DNA analysis were end-labelled with fluorochromes provided by Applied Biosystems (Foster City, CA).

Amplification 1: exons from 5 to 8 of p53 gene (Gene Bank n. X54156, nt. 13042-13253, 13308-13489, 13986-14124, 14404-14603). Amplification 1 and 2: fragments corresponding to aminoacids 862-954 and 1035-1130 of exon 15 of APC gene (Gene Bank AF127506, M74088). Amplification 3 and 4: fragments corresponding to aminoacids 1288-1402 and 1421-1515 of exon 15 of APC gene (Gene Bank AF127506, M74088).

P53	Exons	Primer name	5'-labelling	Sequence
	5	5-F	6-FAM-	ctcttcctgcagtactcccctgc
		5-R		gccccagctgctcaccatcgcta
	6	6-F		gattgctcttaggtctggcccctc
		6-R	HEX	ggccactgacaaccacccttaacc
	7	7-F	6-FAM	gcgttgtctcctaggttggctctg
		7-R		caagtggctcctgacctggagtc
	8	8-F		acctgatttccttactgcctctggc
		8-R	HEX	gtcctgcttgcttacctcgcttagt
APC	**Fragment**	**Primer name**	**5'-labelling**	**Sequence**
	1	1BF		aactaccatccagcaacaga
		1BR	HEX	taatttggcataaggcatag
	2	2F	6-FAM	cagttgaactctggaaggca
		2R		tgacacaaagactggcttac
	3	3F		gatgtaatcagacgacacag
		3R	HEX	ggcaatcgaacgactctcaa
	4	4F	6-FAM	cagtgatcttccagatagcc
		4R		aaatggctcatcgaggctca

Electrophoresis was carried out using a 3100Avant Genetic Analyzer (Applied Biosystems) equipped with GeneScan Analysis 3.7.

FL-DNA was performed by analyzing the fluorescence intensity of each sample-specific PCR product (Fig. 1ab). The quantification of each sample was calculated by reference to a standard curve (1, 2, 5, 10 and 20 ng) of genomic DNA and expressed as nanograms (Fig. 2abc). To verify the presence or absence of Taq inhibitors, an amplification was performed on all samples with a mix containing 2 µl of DNA extracted from stool and 25 attograms [ag] of a plasmid with a control sequence. All determinations were performed in

duplicate and repeated in about 20% of samples in which the variation was >20%.

Case Series

Stool samples from 86 patients with primary colorectal cancer were collected in the Gastroenterology Unit and Dept. of Surgery I, Morgagni Hospital, Forlì and in the Depts. of Oncology and General Surgery, Infermi Hospital, Rimini. Stool samples were collected from 62 individuals who proved negative for cancer or benign lesions after colonoscopy, and from laboratory personnel.

Stool samples were obtained at least three days after the administration of laxative treatments in preparation for colonoscopy to allow for the recovery of normal bowel functionality. The fecal specimens were immediately frozen and stored at –70°C for a maximum of two months.

Cancer diagnosis was histologically confirmed and pathological stage was defined according to Dukes' classification: 8 tumors were classified as stage A, 30 as stage B, 37 as stage C and 9 as stage D. Moreover, 19 cancers were located in ascending, 30 in descending, 2 in transverse colon and 35 in the rectal tract. Staging information was not available for only two cases.

Of the 86 patients, 42 were male and 44 were female and median age was 72 years (range 36-90). Of the 62 controls, 29 were male and 33 female and median age was 51 years (range 21-87).

Results

Fluorescence signals ranged from 0 to 283 ng (median 47 ng) in patient stool and from 0 to 87 ng (median 4 ng) in healthy donor stool. No differences in median values were observed with respect to age of patients and size, site and stage of tumor.

When the results from the two approaches were compared, a direct relation was observed, but with a wide variability of FL-DNA levels within

the subgroups defined according to the number of L-DNA high amplifications. Moreover, fluorescence by FL-DNA method was detected in 33 out of the 47 individuals who did not show any high amplification by L-DNA assay. These results are clearly indicative of a higher sensitivity of the fluorescence method than of the conventional approach.

The ROC curve analysis of FL-DNA levels (Fig. 3) shows a good diagnostic accuracy of this approach. In particular, very high specificity ranging from 83% to 95% and high sensitivity ranging from 82% to 72% were observed for the most discriminant cut-offs of 15, 20, 25 and 30 ng of DNA (Table 1). When the cut-off of 25 ng, which provides the best overall accuracy, was analyzed in relation to the different tumor characteristics, sensitivity remained high in patients with small (70%) compared to large tumors (82%) and was similar for the different Dukes' stage tumors (Table 2). More importantly, a similar sensitivity was observed in detecting tumors localized in ascending and descending colon tracts.

Table 1. Sensitivity and specificity of FL-DNA analysis

DNA LEVELS	HEALTHY DONORS		PATIENTS					
Cut-off (ng)	Positive	Negative	Positive	Negative	Sensitivity %	C.I. 95%	Specificity %	C.I. 95%
15	10	49	70	15	82	(74-90)	83	(73-93)
20	7	52	70	15	82	(74-90)	88	(80-96)
25	4	55	65	20	76	(67-85)	93	(86-100)
30	3	56	61	24	72	(62-82)	95	(89-100)

Table 2. Sensitivity* as a function of different characteristics in colorectal cancer

Category	No. PATIENTS	POSITIVE	NEGATIVE	SENSITIVITY %
SIZE (cm)				
0.1-4.0	40	28	12	70
≥4.1	38	31	7	82
DUKES' STAGE				
A	8	7	1	88
B	29	25	4	86
C	37	25	12	68
D	9	8	1	89
LOCATION				
Ascending	18	13	5	72
Transverse	2	2	0	100
Descending	30	22	8	73
Rectum	35	28	7	80

* Cut off value 25 ng

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CLAIMS

1. A method for determining the presence of colorectal tumors or pre-cancerous lesions in a human subject, which comprises:

a) DNA extraction from stool samples;

b) PCR amplification of at least three different DNA fragments with a length of 100 base pairs or more, using deoxynucleotide triphosphates or primers labelled with detectable markers;

c) quantitation of the amplified fragments (amplicons);

d) calculation of the total amount of different amplicons;

e) comparison of the values obtained in (d) with a reference value.

2. A method according to claim 1, wherein the detectable markers used in step (b) are fluorescent molecules.

3. A method according to claim 2, wherein said fluorescent molecules are selected from HEX, 6-FAM and TAMRA.

4. A method according to claims 1-3, wherein at least 8 different DNA fragments are amplified in step (b).

5. A method according to claim 1, wherein the DNA fragments are from 100 to 500bp.

6. A method according to claim 1, wherein the DNA fragments span different regions of p53 or APC genes.

7. A method according to claim 6, wherein p53 fragments corresponding to exons 5-8 are amplified using the following pairs of primers:

a) ctcttcctgcagtactcccctgc; gccccagctgctcaccatcgcta;

b) gattgctcttaggtctggccccctc; ggccactgacaaccacccttaacc;

c) gcgttgtctcctaggttggctctg; caagtggctcctgacctggagtc;

d) acctgatttccttactgcctctggc; gtcctgcttgcttacctcgcttagt;

8. A method according to claim 6, wherein APC fragments are amplified

using the following pairs of primers:

a) aactaccatccagcaacaga; taatttggcataaggcatag;

b) cagttgaactctggaaggca; tgacacaaagactggcttac;

c) gatgtaatcagacgacacag; ggcaatcgaacgactctcaa;

d) cagtgatcttccagatagcc; aaatggctcatcgaggctca

9. A method according to claims 1-8, wherein the amplicon quantities are interpolated on a calibration curve obtained from known DNA amounts.

10. A method according to claim 1, wherein the amplicons are quantified with an automatic sequencer/analyser or using fluorimetric, colorimetric, radioactive or spectrophotometric detection systems.

11. A method according to claim 1, wherein the reference value is determined on the basis of case series comprising healthy subjects and patients affected by colorectal tumor or lesions.

12. A kit containing oligonucleotides, labelling agents, a thermostable DNA polymerase and user instructions to carry out the method of claims 1-11.

Fig.1a

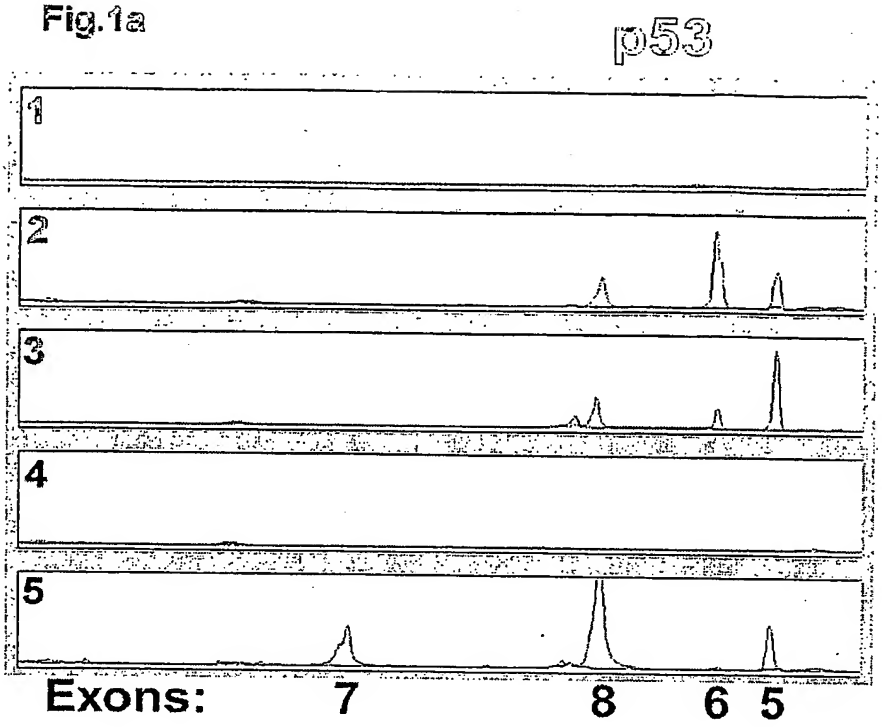


Fig. 1b

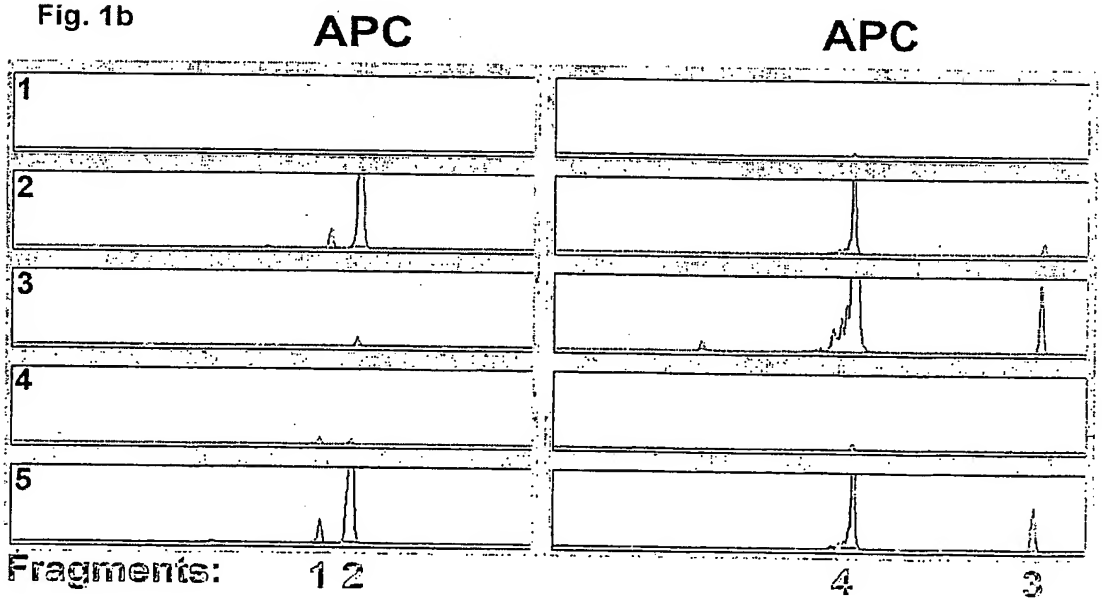
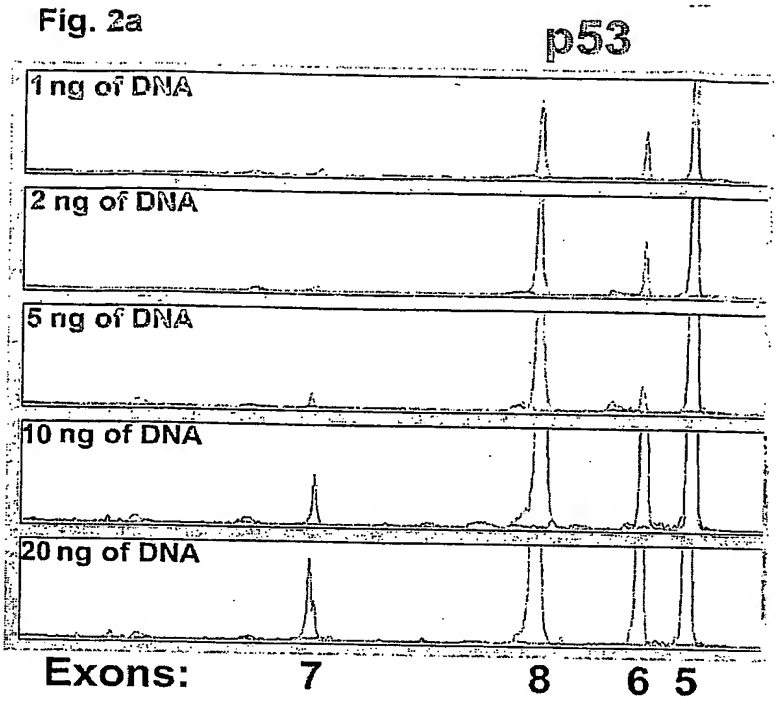


Fig. 2a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5 ng of DNA
10 ng of DNA
20 ng of DNA
Exons: 7 8 6 5

Fig. 2b

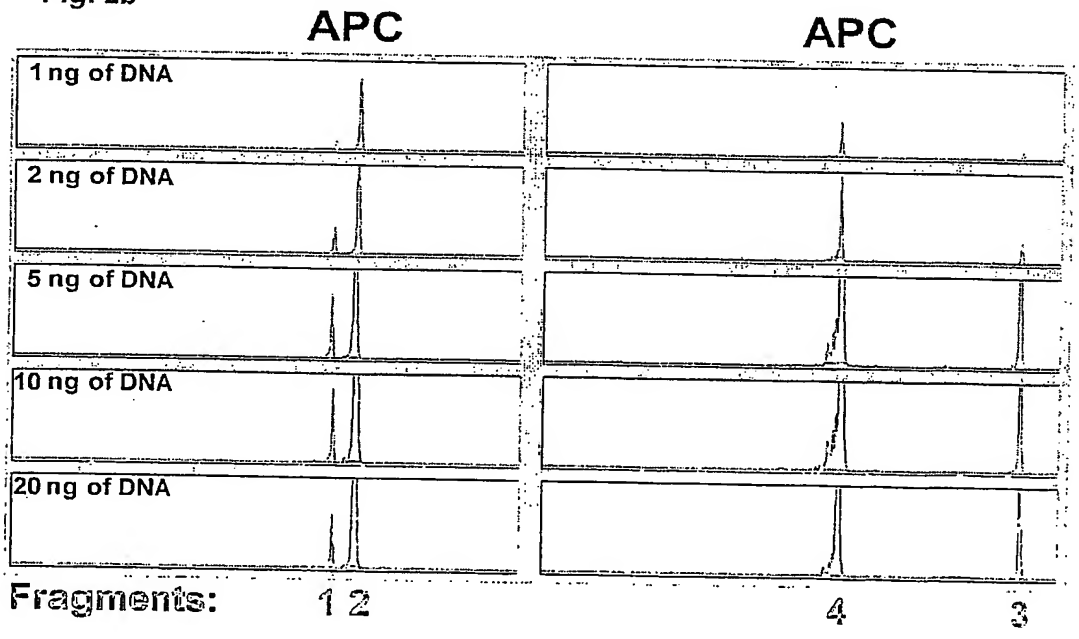
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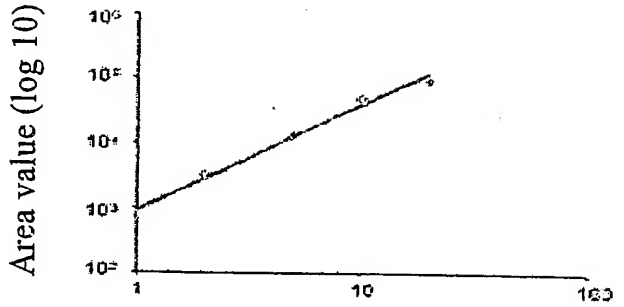
Fig. 2c

p53 curve



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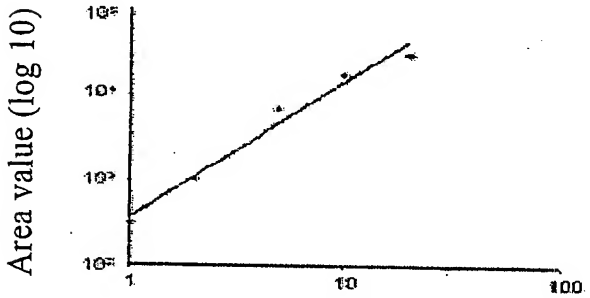

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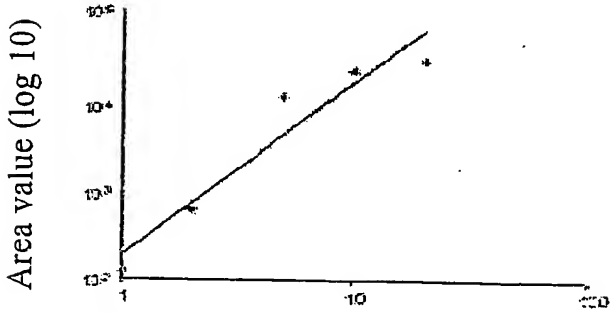
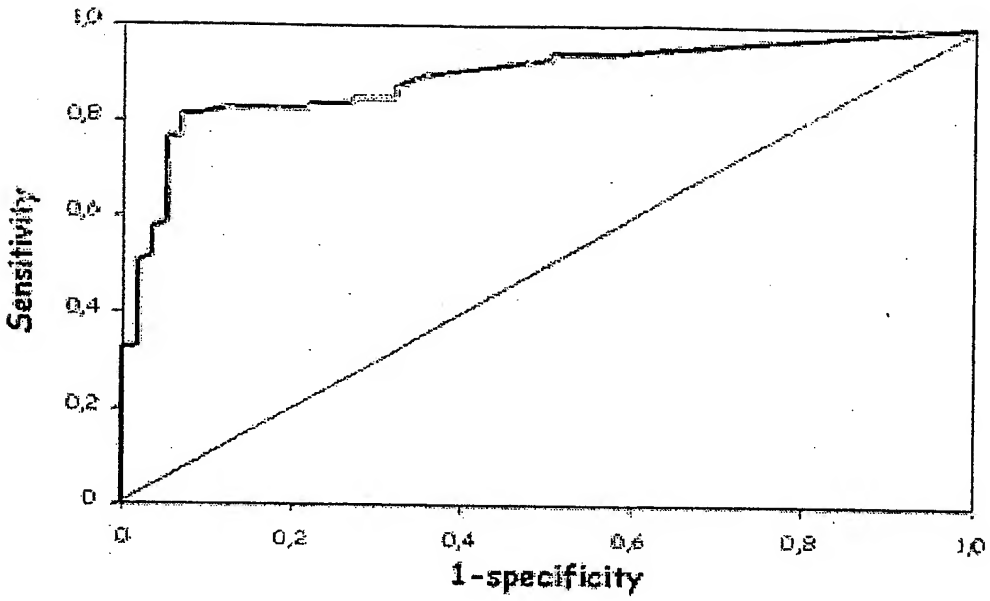


Fig. 3



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INTERNATIONAL SEARCH REPORT

International Application No
PCT/EP2004/001997

A. CLASSIFICATION OF SUBJECT MATTER
IPC 7 C12Q1/68

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)
IPC 7 C12Q

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

EPO-Internal, BIOSIS, WPI Data, PAJ, Sequence Search

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category °	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	WO 01/42502 A (EXACT LAB INC) 14 June 2001 (2001-06-14) the whole document	1-12
X	WO 02/092858 A (EXACT SCIENCES CORP) 21 November 2002 (2002-11-21) the whole document	1-12
X	AHLQUIST D A ET AL: "COLORECTAL CANCER SCREENING BY DETECTION OF ALTERED HUMAN DNA IN STOOL: FEASIBILITY OF A MULTITARGET ASSAY PANEL" GASTROENTEROLOGY, W.B.SAUNDERS COMPANY, PHILADELPHIA, US, vol. 119, no. 5, November 2000 (2000-11), pages 1219-1227, XP001118414 ISSN: 0016-5085 the whole document	1-12

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[X] Further documents are listed in the continuation of box C.

[X] Patent family members are listed in annex.

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Date of the actual completion of the international search	Date of mailing of the international search report
28 June 2004	08/07/2004

Name and mailing address of the ISA	Authorized officer
European Patent Office, P.B. 5818 Patentlaan 2 NL – 2280 HV Rijswijk Tel. (+31-70) 340-2040, Tx. 31 651 epo nl, Fax: (+31-70) 340-3016	Hermann, P

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A	RENGUCCI C ET AL: "Multiple detection of genetic alterations in tumors and stool." CLINICAL CANCER RESEARCH : AN OFFICIAL JOURNAL OF THE AMERICAN ASSOCIATION FOR CANCER RESEARCH. MAR 2001, vol. 7, no. 3, March 2001 (2001-03), pages 590-593, XP002286121 ISSN: 1078-0432 the whole document	1-12
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A	WO 99/06598 A (ONCORMED INC) 11 February 1999 (1999-02-11) Example 6 page 46 (for SEQ. ID. 7)	1-12
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International Application No
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